SEQUENCE LISTING

<110> LALANNE, JEAN L
ROCHER, CORINNE

<120> Novel genes of Candida albicans and the proteins coded by these genes

<130> 146.1374

<140> 09/980,054
<141> 2001-11-28

<150> FR 9907250
<151> 1999-06-09

<150> PCT/FR00/01567
<151> 2000-06-08

<160> 32

<170> PatentIn Ver. 2.1

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<213> Candida albicans

<220>
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Met Ser Asn Asp Asp Ile Ile Leu Pro Ser Val Ser Ser Leu Ser Lys
  1               5                  10                  15

cta act ata aat gat gta tca aaa tca gga ttt gga tac aat ccg tcc   96
Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser
             20                  25                  30

ata gga cca ata tca aat act att acc cta gaa tct tca ctg gta tta   144
Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Leu Val Leu
         35                  40                  45
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tta aat aaa cgt aca ata tca tta aca cca aca tca tct gac tcc att   192
Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile
     50                  55                  60

tat gat aga aat att atc acg aaa aag cca cac gaa atc aac tta tct   240
Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
 65                  70                  75                  80

tcg tta tca ttt ttg ttt tgt gag att att agt tgg gca cac tct aat   288
Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
                 85                  90                  95

tcc aaa ggc att caa gat tta gaa aat cgt tta aac gga tta ggt tat   336
Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
            100                 105                 110

caa ata ggt caa cga tat ctc gaa ttg tgt aaa ata aga gaa ggt ttt   384
Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe
        115                 120                 125

aaa aac agt aaa cga gag att aga ctt ttg gaa atg tta caa ttt att   432
Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile
    130                 135                 140

cat ggt ccg ttc tgg aaa ttg att ttt ggt aaa act gct aat gaa tta   480
His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu
145                 150                 155                 160

gaa aaa tcg caa gat ttg ccc aat gaa tat atg att gtg gag aat gtg   528
Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
                165                 170                 175

cca tta tta aat aga ttt att agt ata cct aag gag tat ggc gac tta   576
Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
            180                 185                 190

aat tgt tca gca ttt gtt gcg ggt ata att gag gga gca ctt gat aat   624
Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
        195                 200                 205

agt gga ttc aat gcc gat gtt aca gca cac acg gtc gct aca gat gca   672
Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
    210                 215                 220

aat cca tta aga aca gta ttt ttg atc aag ttt gac gat tct gtt tta   720
Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu
225                 230                 235                 240
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att aga gag agt ttg aga ttt gga taa                                    747
Ile Arg Glu Ser Leu Arg Phe Gly
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<212> PRT
<213> Candida albicans

<400> 2

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  1               5                  10                  15
Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser
            20                  25                  30
Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Leu Val Leu
        35                  40                  45
Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile
    50                  55                  60
Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
65                  70                  75                  80
Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
                85                  90                  95
Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
            100                 105                 110
Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe
        115                 120                 125
Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile
    130                 135                 140
His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu
145                 150                 155                 160
Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
                165                 170                 175
Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
            180                 185                 190
Asn Lys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
        195                 200                 205
Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
    210                 215                 220
Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu
225                 230                 235                 240
Ile Arg Glu Ser Leu Arg Phe Gly
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<213> Candida albicans

<220>
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Met Asp Ile Asp Asp Ile Leu Lys Glu Phe Glu Glu Ser Ser Lys Asp
  1               5                  10                  15

gaa aag att agc agt aaa aca tcg tct atc aac tta tat caa gac ttg    96
Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu
             20                  25                  30

cta aga gct atg atc aac gaa cgt atg gct ccg gaa tta ttg cca tac   144
Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr
         35                  40                  45

aaa caa gat tta atg tcc act gtt tta aca atg atg tct aac caa caa   192
Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln
     50                  55                  60

caa tat tta tta gaa tct cac gaa tat ggt gat atg aat ggc gac agt   240
Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser
 65                  70                  75                  80

ggt gta tta tcc gga gac ttt aaa tta caa cta atg att atc gaa act   288
Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr
                 85                  90                  95

gat tta gag cgt ctc aac tat att gtt cga tta tac ata cga act cga   336
Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg
            100                 105                 110

ttg agt aag ttg aat aaa ttt act att ttt tac atc aat gaa agc agt   384
Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser
        115                 120                 125

caa aat gat aat tta ttg tcc aaa gag gaa aga gat tat ata cac aaa   432
Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys
    130                 135                 140
```

```
tat ttc cag att ttg act caa tta tat aac aac tgt ttc ctc aaa aaa   480
Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys
145                 150                 155                 160

cta cca caa atg ttg acc tat ttg gat gac acc agt ggt gga caa tca   528
Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser
                165                 170                 175

atg atc gtt gag cca gat tta gac cag cct gtg ttt atc aaa tgt acc   576
Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr
            180                 185                 190

ctg gaa gtc cca ata tta cta gat tac gac ggt gct aca gag ata gat   624
Leu Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp
        195                 200                 205

tta gaa tta ata aaa aag gga gtc tac gtg gtg aaa tac agc cta gtc   672
Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val
    210                 215                 220

aaa aga tat att gat att gga gat gtg gta ttg ata tga               711
Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile
225                 230                 235
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<210> 4
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<212> PRT
<213> Candida albicans

<400> 4

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Met Asp Ile Asp Asp Ile Leu Lys Glu Phe Glu Glu Ser Ser Lys Asp
  1               5                  10                  15
Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu
            20                  25                  30
Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr
        35                  40                  45
Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln
    50                  55                  60
Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser
65                  70                  75                  80
Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr
                85                  90                  95
Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg
            100                 105                 110
Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser
        115                 120                 125
```

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Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys
    130                 135                 140
Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys
145                 150                 155                 160
Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser
                165                 170                 175
Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr
            180                 185                 190
Leu Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp
        195                 200                 205
Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val
    210                 215                 220
Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile
225                 230                 235
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<210> 5
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<213> Candida albicans

<220>
<221> CDS
<222> (1)..(1383)

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  1               5                  10                  15

gaa cca acc cca aaa ccc aca att ggt gga ttc ccc gaa ctt aaa aaa   96
Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
             20                  25                  30

tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa caa cag gaa  144
Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
         35                  40                  45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc  192
Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
     50                  55                  60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa  240
Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65                  70                  75                  80

gag att ttg caa gag cgt gag gag tta cta aag ggt tta gat cct aaa  288
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```
Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
                 85                  90                  95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac   336
Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
            100                 105                 110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga   384
His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
        115                 120                 125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa   432
Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
    130                 135                 140

tta gat aag gaa gat gtg gac cgt gca ttg ggt ata agt tca tta tcc   480
Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145                 150                 155                 160

tta tct gaa cct gag ggt ggc agt aat acg aaa aaa gtc gct ttc gac   528
Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
                165                 170                 175

gat aat atc aag acg gtt aaa ttt gaa gat ttg gat gat gga att gaa   576
Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
            180                 185                 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt   624
Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
        195                 200                 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat   672
Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
    210                 215                 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa   720
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225                 230                 235                 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat   768
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
                245                 250                 255

gag aaa tat tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg   816
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
            260                 265                 270

atg aca cag cta atg cca aaa caa ttg tct acc gtt tat gaa tca ata   864
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Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
        275                 280                 285

tct gat atg aga ttt gac ttt aaa gga gat tta att gaa ttg ggt cca   912
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
    290                 295                 300

gag gga gaa gaa cca aaa gat agt tca tcc gaa ata cct act tat atg   960
Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
305                 310                 315                 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg  1008
Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
                325                 330                 335

ggt gag ttg gca cat tta gcc aga tcg act tta gct gga caa aga tgc  1056
Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
            340                 345                 350

ttg agc att caa aca tta ggg aga atc tta cat aaa ttg gga tta cat  1104
Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
        355                 360                 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca  1152
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
    370                 375                 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac  1200
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385                 390                 395                 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat  1248
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
                405                 410                 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca  1296
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
            420                 425                 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa  1344
Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
        435                 440                 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa              1383
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
    450                 455                 460
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<213> Candida albicans

<400> 6

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Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
            20                  25                  30
Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
        35                  40                  45
Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
    50                  55                  60
Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65                  70                  75                  80
Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
                85                  90                  95
Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
            100                 105                 110
His Gln His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
        115                 120                 125
Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
    130                 135                 140
Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145                 150                 155                 160
Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
                165                 170                 175
Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
            180                 185                 190
Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
        195                 200                 205
Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
    210                 215                 220
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225                 230                 235                 240
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
                245                 250                 255
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
            260                 265                 270
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
        275                 280                 285
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
    290                 295                 300
Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
305                 310                 315                 320
Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
                325                 330                 335
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```
Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
            340                 345                 350
Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
        355                 360                 365
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
    370                 375                 380
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385                 390                 395                 400
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
                405                 410                 415
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
            420                 425                 430
Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
        435                 440                 445
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
    450                 455                 460
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<210> 7
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<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(1380)

<400> 7

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Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
  1               5                  10                  15

gaa cca acc cca aaa ccc aca att ggt gga ttc ccc gaa ctt aaa aaa   96
Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
             20                  25                  30

tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa caa cag gag   144
Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
         35                  40                  45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc   192
Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
     50                  55                  60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa   240
Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65                  70                  75                  80
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gag att ttg caa gag cgt gag gag tta cta aag ggt tta gac cct aaa   288
Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
                85                  90                  95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac   336
Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
            100                 105                 110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga   384
His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
        115                 120                 125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa   432
Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
    130                 135                 140

tta gat aag gaa gat gtg gac cgt gct ttg ggt ata agt tca tta tcc   480
Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145                 150                 155                 160

tta tct gaa cct gag ggt ggc agc aat acg aaa aaa gtc gct ttc gac   528
Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
                165                 170                 175

gat aat atc aag acg gtt aaa ttt gaa gct ttg gat gat gaa att gaa   576
Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
            180                 185                 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt   624
Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
        195                 200                 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat   672
Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
    210                 215                 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa   720
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225                 230                 235                 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat   768
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
                245                 250                 255

gag aaa tat tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg   816
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
            260                 265                 270
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atg aca cag cca atg cca aaa caa ttg tct aca gtt tat gaa tca ata   864
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
        275                 280                 285

tct gat atg aga ttt gac ttc aaa gga gat tta att gaa ttg agc gca   912
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
    290                 295                 300

gag gga gaa gaa cca aaa gat agt tca ttc gaa ata cct act tat atg   960
Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
305                 310                 315                 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg  1008
Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
                325                 330                 335

ggt gag ttg gca cat tta gcc aga tcg act tta gct gga caa aga tgc  1056
Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
            340                 345                 350

ttg agc att caa aca tta ggg aga ata tta cat aaa ttg gga tta cat  1104
Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
        355                 360                 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca  1152
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
    370                 375                 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac  1200
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385                 390                 395                 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat  1248
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
                405                 410                 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca  1296
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
            420                 425                 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa  1344
Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
        435                 440                 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa              1383
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
    450                 455                 460
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<210> 8
<211> 460
<212> PRT
<213> Candida albicans

<400> 8

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Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
  1               5                  10                  15

Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
            20                  25                  30

Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
        35                  40                  45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
    50                  55                  60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65                  70                  75                  80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
                85                  90                  95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
            100                 105                 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
        115                 120                 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
    130                 135                 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145                 150                 155                 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
                165                 170                 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
            180                 185                 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
        195                 200                 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
```

210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
450 455 460

<210> 9
<211> 2262
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(2262)

<220>
<221> modified_base
<222> (1093)..(1095)

<220>
<221> modified_base
<222> (1828)..(1830)

<400> 9

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atg gca gca gca cca cca cca cca gcg aaa aac cag ggt aag gca aaa   48
Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys
  1               5                  10                  15

cag cat gtt aca ggt gcc agg ttc cgt cag cga aaa atc tcg gta aag   96
Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
             20                  25                  30

cag ccc ttg act att tat aaa cag aga gac cta cct act cta gat agc   144
Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser
         35                  40                  45

aat gag tta gag cct agt caa gtc cat cat tta aat tct aat gcg tca   192
Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser
     50                  55                  60

tca tca tca aca caa caa ccg aga gac ctt cat gca gtt gaa act ggg   240
Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly
 65                  70                  75                  80

gtt gac aag aat gag gaa gag gaa gtg cat ctt cag caa gtt atc aat   288
Val Asp Lys Asn Glu Glu Glu Glu Val His Leu Gln Gln Val Ile Asn
                 85                  90                  95

gct gca caa aaa gca ctt ttg ggt tcg aaa aaa gaa gaa aaa agc agt   336
Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser
            100                 105                 110

gat atg tat att ccc aca ccg gac gct tcg agg ata tgg ccc gag gca   384
```

```
Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala
        115                 120                 125

cac aag tat tac aag gat caa aag ttc aag cag cca gag aca tat atc   432
His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile
    130                 135                 140

aag ttt agt gcg aca gta gag gac aca gtg ggt gtg gag tac aat atg   480
Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met
145                 150                 155                 160

gac gag gta gat gaa aag ttt tat aga gag aca cta tgc aag tac tat   528
Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr
                165                 170                 175

ccc aaa aag aaa aac aag tca gat gag aac aat cga aag tgt act gaa   576
Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu
            180                 185                 190

ttg gag ttt gaa aca atc tgt gac aag ttg gaa aag acc att gaa gca   624
Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala
        195                 200                 205

cga caa ccg ttt ttg tct atg gac ccc agc aac att cta tcg tac gag   672
Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu
    210                 215                 220

gag ttg tcg tcg tac att gtg gat cag ttt aaa agt gca gtg aaa aca   720
Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr
225                 230                 235                 240

agc aac ccg tat att gtt acc aat ggt ggg aat cta gag tat ata tcg   768
Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser
                245                 250                 255

acg aca gct tta aaa gag aga ttg tcg aag gaa ata aag tat gaa ccg   816
Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro
            260                 265                 270

ttt gtt act att ttt gat aag aac caa atg tcc aca agt gcg gtg aga   864
Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg
        275                 280                 285

cct att ccc aaa ttg ttt gag ttg ttc ggc aga cct gtt tat gat cat   912
Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His
    290                 295                 300

tgg aag gag aga aaa ata gaa aga aag ggc aaa acc atc cag ccc aca   960
```

```
Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr
305                 310                 315                 320

ctc aaa ttt gag gat cct aac tcg aac gaa aag gaa aac gac aat gac   1008
Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp
                325                 330                 335

cca tat ata tgt ttc aga cga cgt gag ttt agg caa gca aga aag acg   1056
Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr
            340                 345                 350

aga aga gcc gat aca att ggt gca gag aga ata aga ctg atg caa aag   1104
Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Leu Met Gln Lys
        355                 360                 365

tcg ttg cac cgc gca cgt gat ttg ata atg agt gtt agt gaa aga gag   1152
Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu
    370                 375                 380

atc ctc aaa ctc gac aat ttt caa gca gag cat gaa ttg ttt aaa gcc   1200
Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala
385                 390                 395                 400

agg tgc gct acc aag gct tgt aag agg gag ctc aat atc aag ggt gac   1248
Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp
                405                 410                 415

gaa tac ttg ttc ttt ccg cat aaa aag aag aaa att gtt cgt act gaa   1296
Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Lys Ile Val Arg Thr Glu
            420                 425                 430

gat gaa gaa agg gag aag aag aga gaa aag aag aag caa gac caa gaa   1344
Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu
        435                 440                 445

ctt gca ctc aag caa caa caa gca cta cag caa cag cag caa caa cca   1392
Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Gln Pro
    450                 455                 460

cca caa cca cca caa caa gca cca tca aaa caa gat ggt aca tca acg   1440
Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr
465                 470                 475                 480

agc cag cct tat gtc aaa ctc cca ccc gca aaa gtt cca gat atg gat   1488
Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp
                485                 490                 495

ctt gtt aca gtt tcg ttg gta tta aag gaa aag aac gaa acc atc aaa   1536
```

```
Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys
            500                 505                 510

cgt gct gtg ttg gag aaa ttg cgc aag aga aag gaa cac gac aag gga  1584
Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly
        515                 520                 525

ttt atc aat ttg aca gac gat ccg tat cag cca ttt ttc gat att tca  1632
Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser
    530                 535                 540

acc aat agg gcc gaa gag ttg agc cat att ccg tat tcg tcg att gcg  1680
Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala
545                 550                 555                 560

gcc aca cac tat cac caa ttc aac aca tcg aac tac atg aac gac caa  1728
Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln
                565                 570                 575

ctt aaa aag cta ctt gaa gag aaa aaa cct tta cct ggt gta aaa acg  1776
Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr
            580                 585                 590

ttt ttg ggt tct aac ggg gag ttg gta cca tcg aag gca ttt cca cat  1824
Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His
        595                 600                 605

ttg ctg tcg ttg ctt gag gaa aag tat aag gcg aca agt ggg tat att  1872
Leu Leu Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile
    610                 615                 620

gaa cga tta ttg caa agc gtg gag acg caa gat ttt agt tca tac acc  1920
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr
625                 630                 635                 640

aat ggc ttt aaa gat gtt gag cca aaa gaa aca aat gaa cct gtt atg  1968
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met
                645                 650                 655

gcg ttt ccc cag aga ata cgt cga aga gtg ggc agg gct ggc agg gtt  2016
Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val
            660                 665                 670

ttt ttg gac cac cag caa gag tac ccg caa ccg aat ttt cag caa gac  2064
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp
        675                 680                 685

aca gat cgt gtg gga ggt atc cca gat gtg tat tgt aaa gag gat gcc  2112
```

```
Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala
    690                 695                 700

att aaa cga tta cag tca aag tgg aag ttc gat aca gaa tat aaa aca   2160
Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr
705                 710                 715                 720

act gaa cca ttt agt ttg gat cct tca aag ttg aat ggt att agt cca   2208
Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro
                725                 730                 735

tct acg caa tcg att aga ttt ggg tct atg ttg ttg aat aga aca cgt   2256
Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg
            740                 745                 750

aaa tag                                                          2262
Lys
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<210> 10
<211> 753
<212> PRT
<213> Candida albicans

<400> 10

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Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys
  1               5                  10                  15
Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
            20                  25                  30
Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser
        35                  40                  45
Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser
    50                  55                  60
Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly
65                  70                  75                  80
Val Asp Lys Asn Glu Glu Glu Glu Val His Leu Gln Gln Val Ile Asn
                85                  90                  95
Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser
            100                 105                 110
Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala
        115                 120                 125
His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile
    130                 135                 140
Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met
145                 150                 155                 160
Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr
                165                 170                 175
Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu
```

```
                180                 185                 190
Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala
        195                 200                 205
Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu
    210                 215                 220
Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr
225                 230                 235                 240
Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser
                245                 250                 255
Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro
            260                 265                 270
Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg
        275                 280                 285
Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His
    290                 295                 300
Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr
305                 310                 315                 320
Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp
                325                 330                 335
Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr
            340                 345                 350
Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Leu Met Gln Lys
        355                 360                 365
Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu
    370                 375                 380
Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala
385                 390                 395                 400
Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp
                405                 410                 415
Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Lys Ile Val Arg Thr Glu
            420                 425                 430
Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu
        435                 440                 445
Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Gln Pro
    450                 455                 460
Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr
465                 470                 475                 480
Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp
                485                 490                 495
Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys
            500                 505                 510
Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly
        515                 520                 525
Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser
    530                 535                 540
Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala
545                 550                 555                 560
Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln
```

```
                565                 570                 575
Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr
            580                 585                 590
Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His
        595                 600                 605
Leu Leu Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile
    610                 615                 620
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr
625                 630                 635                 640
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met
                645                 650                 655
Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val
            660                 665                 670
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp
        675                 680                 685
Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala
    690                 695                 700
Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr
705                 710                 715                 720
Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro
                725                 730                 735
Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg
            740                 745                 750
Lys
```

<210> 11
<211> 447
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(447)

<400> 11

```
atg tca gat ata gat ata gat aat gta tta aat tta gaa gaa gaa caa    48
Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Glu Gln
  1               5                  10                  15

tat gaa tta gga ttt aaa gaa ggt caa ata caa gga aca aaa gat caa    96
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln
             20                  25                  30

tat tta gaa gga aaa gaa tat ggt tat caa act gga ttt caa cga ttt   144
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe
         35                  40                  45
```

```
tta atc att ggt tat att caa gaa tta atg aaa ttt tgg tta tcc cat   192
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His
     50                  55                  60

ata gat caa tat aat aac tct tct tca ctt cgg aat cat ttg aat aat   240
Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn
 65                  70                  75                  80

ttg gaa gat att atg gca caa att tct ata acg aat gga gat aaa gaa   288
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu
                 85                  90                  95

gtt gaa gat tat gaa aaa aat att aaa aag gca aga aat aaa tta aga   336
Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg
            100                 105                 110

gtg ata gct agt ata act aaa gaa act tgg aaa att gat tca ttg gat   384
Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
        115                 120                 125

aat ttg gtg aaa gaa gta ggt gga act tta caa gtt agt gaa aac ccc   432
Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
    130                 135                 140

gat gat atg tgg tga                                             447
Asp Asp Met Trp
145
```

<210> 12
<211> 148
<212> PRT
<213> Candida albicans

<400> 12

```
Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Glu Gln
  1               5                  10                  15
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln
             20                  25                  30
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe
         35                  40                  45
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His
     50                  55                  60
Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn
 65                  70                  75                  80
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu
                 85                  90                  95
```

```
Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg
            100                 105                 110
Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
        115                 120                 125
Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
    130                 135                 140
Asp Asp Met Trp
145
```

<210> 13
<211> 966
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(966)

<400> 13

```
atg ggt aaa aga aga gta gat gaa gaa tct gat tca gat att gat gtt   48
Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
  1               5                  10                  15

agt tca acc gat tca gaa act gaa tta gaa agc aca caa caa caa caa   96
Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln
             20                  25                  30

caa caa caa gaa ggt gct act aca att caa gaa act gtt gat gtt gat   144
Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
         35                  40                  45

ttt gat ttt ttt gat tta aat cct caa att gat ttc cat gct act aag   192
Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
     50                  55                  60

aat ttt tta aga caa tta ttt ggt gat gat aat gga gaa ttt aat tta   240
Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
 65                  70                  75                  80

agt gaa ata gcc gat tta att tta cga gaa aat tcc gtg ggg aca tca   288
Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
                 85                  90                  95

att aaa act gaa gga atg gaa agt gat cca ttt gca att tta agt gta   336
Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
            100                 105                 110
```

```
att aat tta act aat aat tta aat gtg gcc gtg att aaa caa ttg att   384
Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile
        115                 120                 125

gaa tat att tca aat aaa acc aaa tct aaa act gaa ttc aat att att   432
Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile
    130                 135                 140

ttg aaa aaa ttg tta acc aat cag aac gat act act aga gat agg aaa   480
Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys
145                 150                 155                 160

ttt aaa act gga tta ata att agt gaa aga ttt ata aat atg cca gtt   528
Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val
                165                 170                 175

gaa gtg att cca cca atg tat aaa atg ctt tta caa gaa atg gaa aaa   576
Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys
            180                 185                 190

gct gaa gat gct cat gaa aat tat gaa ttt gat tat ttt tta att ata   624
Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
        195                 200                 205

tca aga gtt tat caa tta gtt gat cca gtg gaa aga gaa gat gaa gat   672
Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
    210                 215                 220

cac gaa aaa gaa tcc aat cgt aaa aag aag aac aag aat aag aag aag   720
His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Asn Lys Lys Lys
225                 230                 235                 240

aaa ttg gct aat aat gaa cca aaa cca ata gaa atg gat tat ttc cat   768
Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
                245                 250                 255

ctt gaa gat caa att ttg gaa tca aat act caa ttt aaa gga ata ttt   816
Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe
            260                 265                 270

gaa tat aat aat gaa aat aaa caa gaa aca gat tca aga aga gta ttt   864
Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
        275                 280                 285

act gaa tat ggt att gat cct aaa tta agt tta atc tta att gat aaa   912
Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
    290                 295                 300
```

```
gat aat tta gct aaa tca gtc att gaa atg gaa caa caa ttc cca cct   960
Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
305                 310                 315                 320

cca taa                                                          966
Pro
```

<210> 14
<211> 321
<212> PRT
<213> Candida albicans

<400> 14

```
Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
  1               5                  10                  15
Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln
             20                  25                  30
Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
         35                  40                  45
Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
     50                  55                  60
Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
 65                  70                  75                  80
Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
                 85                  90                  95
Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
            100                 105                 110
Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile
        115                 120                 125
Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile
    130                 135                 140
Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys
145                 150                 155                 160
Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val
                165                 170                 175
Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys
            180                 185                 190
Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
        195                 200                 205
Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
    210                 215                 220
His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Asn Lys Lys Lys
225                 230                 235                 240
Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
                245                 250                 255
Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe
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            260                 265                 270
Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
        275                 280                 285
Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
    290                 295                 300
Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
305                 310                 315                 320
Pro
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<210> 15
<211> 320
<212> DNA
<213> Candida albicans

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aaatcgcaag atttgcccaa tgaatatatg attgtggaga atgtgccatt attaaataga 120
tttattagta tacctaagga gtatggcgac ttaaattgtt cagcatttgt tgcgggtata 180
attgagggag cacttgataa tagtggattc aatgccgatg ttacagcaca cacggtcgct 240
acagatgcaa atccattaag aacagtattt ttgatcaagt ttgacgattc tgttttaatt 300
agagagagtt tgagatttgg   320

<210> 16
<211> 295
<212> DNA
<213> Candida albicans

<400> 16
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attgagtaag ttgaataaat ttactatttt ttacatcaat gaaagcagtc aaaatgataa 120
tttattgtcc aaagaggaaa gagattatat acacaaatat ttccagattt tgactcaatt 180
atataacaac tgtttcctca aaaaactacc acaaatgttg acctatttgg atgacaccag 240
tggtggacaa tcaatgatcg ttgagccaga tttagaccag cctgtgttta tcaaa   295

<210> 17
<211> 342
<212> DNA
<213> Candida albicans

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atctctgata tgagatttgg ctttaaaggc gatttaattg aattggctcc agtgggagat 60
gcaccaaaag atagttcatc cgacatacgt actcatatgg gactccatca tcattcggag 120
accccagata tggcaggtta tacattgggt gagttggccc atttagccag atcgacttta 180
gctggacaaa gatgcttgag cattcaaaca ttagggagaa tcttccataa attgggatta 240

catnaatata gtatactatc aaaccagctc aatgatcaga gttttacaga tgaatcaaaa 300
ctatcacttg actttgaaga tagatgtggg atttgataga ccaattacga atcattgaaa 360
caataacaga ggcagttgat ggaaaaaaga cc 392

<210> 18
<211> 335
<212> DNA
<213> Candida albicans

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attctcacac cggacgcttc gaggatatgg cccgaggcac acaagtatta caaggatcaa 60
aagttcaagc agccagagac atatatcaag tttagtgcga cagtagagga cacagtgggt 120
gtggagtaca atatggacga ggtagatgaa aagttttata gagagacact atgcaagtac 180
tatccaaaaa agaaaaacaa gtcagatgag aacaatcgaa agtgtactga attggagttt 240
gaaacaatct gtgacaagtt ggaaaagacc attgaagcac gacaaccgtt tttgtctatg 300
gaccccagca acattctatc gtacgaggag ttgtc 335

<210> 19
<211> 326
<212> DNA
<213> Candida albicans

<400> 19
agatatagat aatgtattaa atttagaaga agatcaatat gaattaggat ttaaagaagg 60
tcaaatacaa ggaacaaaag atcaatattt agaaggaaaa gaatatggtt atcaaactgg 120
attcaacga ttttttaatca ttggttatat tcaagaatta atgaaatttt ggttatccca 180
tatagatcaa tataataact cttcttcact tcggaatcat ttgaataatt tggaagatat 240
tatggcacaa atttctataa cgaatggaga taaagaagtt gaagattatg aaaaaaatat 300
taaaaaggca agaaataaat taagag 326

<210> 20
<211> 374
<212> DNA
<213> Candida albicans

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cttaaaattg atttccatgc tactaagaat ttttaagaca ttatttggtg atgataatgg 60
agaatttaat ttaagtgaaa tagccgattt aattttacga gaaaattccg tggggacatc 120
aattaaaact gaaggaatgg aaagtgatcc atttgcaatt ttaagtgtaa ttaatttaac 180
taataattta aatgtggccg tgattaaaca attgattgaa tatatttttaa ataaaaccaa 240
atctaaaact gaattcaata ttatttttgaa aaaattgtta accaatcaga acgatactac 300
tagagatagg aaatttaaaa ctggattaat aattagtgaa agatttataa atatgccagt 360
tgaagtgatt ccac 374

<210> 21
<211> 35
<212> DNA
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<220>
<221> modified_base
<222> (18)
<223> n=a or g or c or t

<400> 21
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<210> 22
<211> 29
<212> DNA
<213> Candida albicans

<400> 22
ccaaaatctca aactctctct aattaaaac 29

<210> 23
<211> 38
<212> DNA
<213> Candida albicans

<400> 23
gttcatgrtt ggtgactcag agcgtctcaa ctatattg 38

<210> 24
<211> 33
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<400> 24
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<210> 25
<211> 32
<212> DNA
<213> Candida albicans

<400> 25
atctctgata tgagatttgg ctttaaaggc ga 32

<210> 26
<211> 32
<212> DNA
<213> Candida albicans

<400> 26
ggtcttttct ccatcagctg cctctgttat tg 32

<210> 27
<211> 20
<212> DNA
<213> Candida albicans

<400> 27
attcccacac cggacgcttc 20

<210> 28
<211> 20
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<213> Candida albicans

<400> 28
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<210> 29
<211> 20
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<213> Candida albicans

<400> 29
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<210> 30
<211> 20
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<213> Candida albicans

<400> 30
ctcttaattt atttcttgcc 20

<210> 31

<211> 20
<212> DNA
<213> Candida albicans

<400> 31
cctcaaattg atttccatgc 20

<210> 32
<211> 20
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<213> Candida albicans

<400> 32
gtggaatcac ttcaactggc 20